



Figure 1C

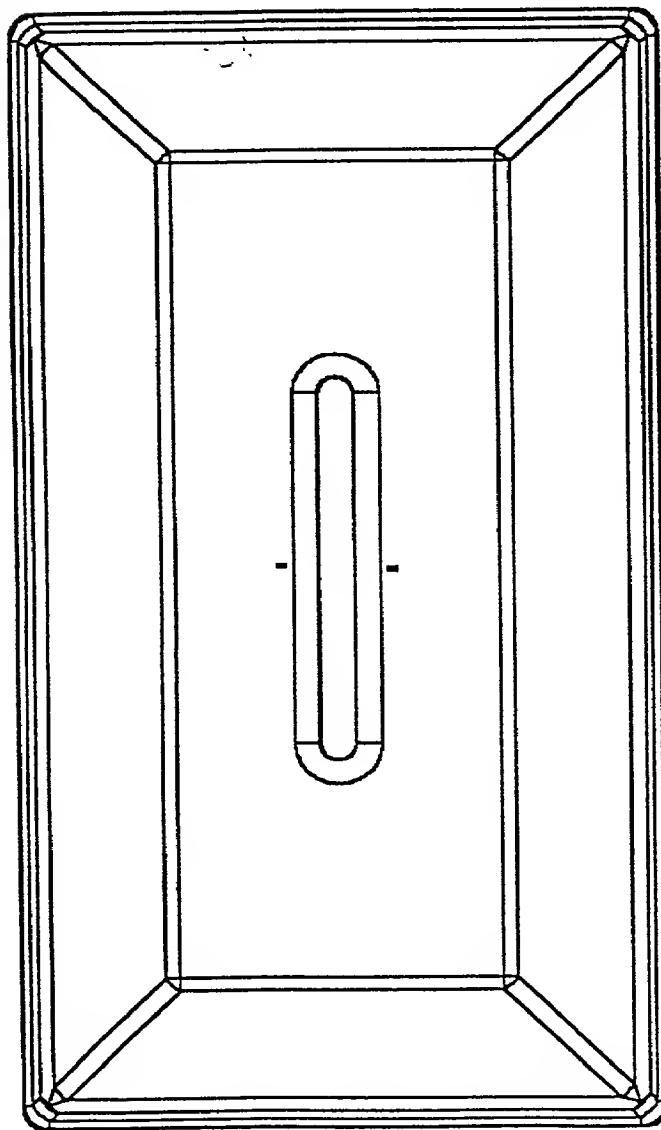


Figure 1A



Figure 1B

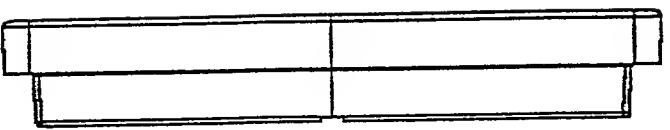


Figure 2C

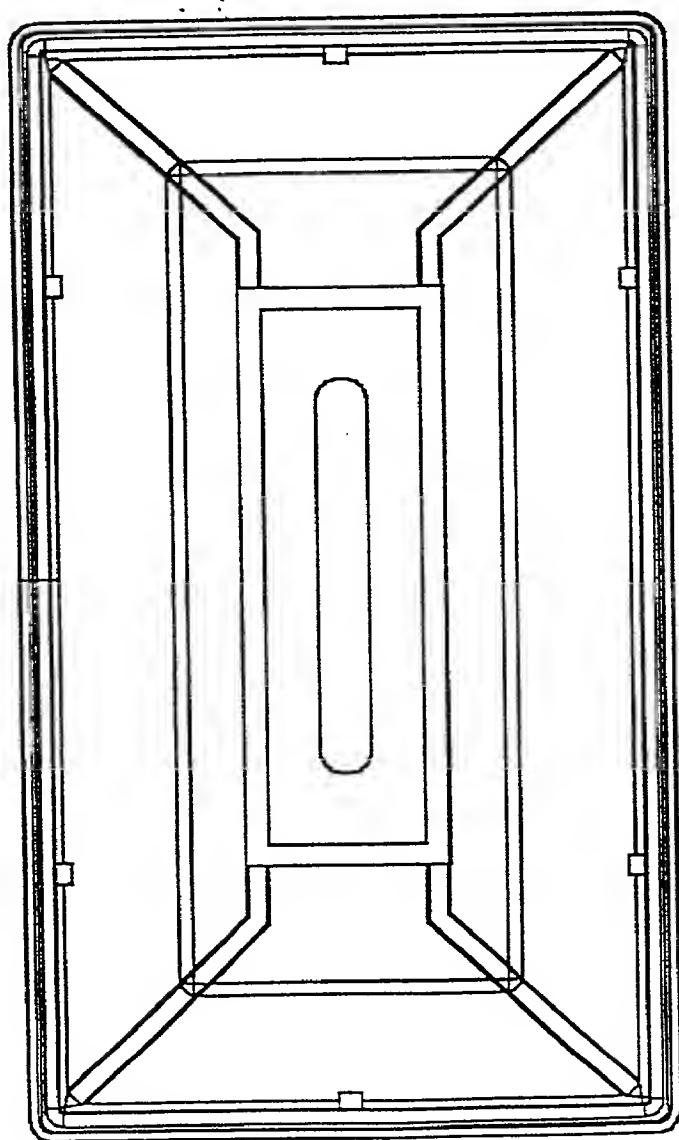


Figure 2A

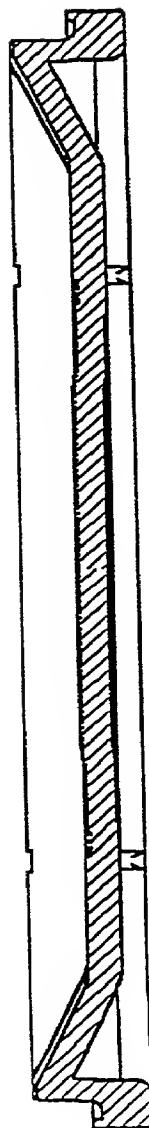


Figure 2B

Figure 3A

Nucleotide sequence of *Cryptosporidium parvum* protein disulfide isomerase cDNA

5

001 atgatcgaa ttagaagctt gttttcagca gcatttttag gtttttcttg tctctcccaag
061 gtagtctgg gtggagatga agtcacttc attcagaac acattactc cttaaacttcc
121 tccaaacttcg aagacttcat taaggagaag gaacacgtaa ttgttactt cttggccca
181 tggtgccgc attgtactgc tttagggca gaattcaagg caacatgcg tgaaatctca
241 aagctcttc ccccagtaca ctgtggcagt gttgatgcaa ctgaaaatat ggagcttgc
301 caacaatatg gtgtggcgg atacccaaacc atcaaaattt tcagtggat tgacagtgtt
361 cagaactatt caggagaag aagcaaggat gcattcatca agtattaa gaagttgacc
421 ggaccaggcg tccaaagtgc tgaatcagaa gaagctatca agacaatctt cgcttcttct
481 tcttcagcct ttgttggaaatttccatc aaggactcag ctgaggtatgc tgcaggatgc
541 aagtttgcg tgggtcacccg cggcacaaac tatgccttca ttgtttctt ccaagaaggat
601 gaacaaagg tcgaggattt acacaaggac gaggaggccag ttcttccc aatgccaagg
661 actgttgaag agttggggc caagatatcc ataatgttgc taccattgtt ctctgcaatt
721 agtgcgtgaga actactccc ctatatgtca agagaaaggat atactgcctgg ttctgtggta
782 ctaacgagga cttcgccaaag tatgttcaaa acattagaaa acattagaaa ggttgcagc
842 aaaagtatgc cttgttttc ctgtatctt gggcaatttgc gttcccatgc tactcaacat
901 ctcttaattt gaaaattcc agttttggtt atccaaatgt tcaatgttcc atcaattaga
961 tacatgtatg gtccaggctaa attcgactt gttgagccat taaaggaaat tatgaagccaa
1021 gtttctgaaag gcaaggcacaactcaggatt aagtctgagg caatcccagg tgaggcaatct
1081 ggtccagtc ctgttgcgtt tgtaaggacc ttcgaaagaaa ttgtttcag aagtgacaag
1141 gatgttctt tggaaatcta tgcccaatgg tggacact gtaaggaaat cggccaaatc
1201 tacaaaccac tcggcgaaga gtacaaggac aacgacaagg ttgtgattgc aaagatcaat
1261 ggaccacaaa acgatatccc atatgaaagg ttcagtccaa gaggcctccc aactatctg
1321 ttcgtaagg ccggaaacttag aaccctaaatt ctttatgtg gaaaggaaac tggaggcc
1381 ttcaaggaaat tcattatgtg acatcgttcaag aaaaggaaatc tcgtgacgaa
1441 ctctaa

20

25

30

Figure 3B

Deduced Amino Acid Sequence of *C. parvum* Protein Disulfide Isomerase

5 MIGIRSLVSAAFLGGFSCLSKVVLGGDEAHFISEHITSLTSSSNFEDFIKSKEEHVIVTFFAP
61 WCGHCTALEPERFKATCAEISKLSSPPVHCGSVDATENMELAQYGVSGYPTIKFFSGIDSV
121 QNYSGARSKDAFIKYIKKLTGPAVQVAESEEAIKTIASSSSAFVGRFTSKDSAEYAVFE
181 KVASGHREHNYAFIAFFQEQQKLEVLHKDEEPVSLPMPKTVEELEAKISIMNVPLFSAI
241 SAENYSLYMSREGYTAWFCCGTNEDFAKYASNIRKVAADYREKYAFVFLDTEQFGSHATQH
301 LLIEKFPGLVIQSVNVPSIRYMYGPAKFDSSVEPLKEFMKQVSEGKHLSIKSEPIPAEQS
361 GPVTVVVGKTFEEIVFRSDKDVILLEIYAQWCGHCKNLEPIYNQLGEEYKDNDKVVIAKIN
421 GPQNDIIPYEGFSPRAFPITLFWKAGTRTPIPYDGKRTVEAFKEFISEHSSFPQEKECSRDEL